

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Pulst, Stefan M.
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 - (B) STREET: 444 South Flower Street, Suite 2000
 - (C) CITY: Los Angeles
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ramos, Robert T.
 - (B) REGISTRATION NUMBER: 37,915
 - (C) REFERENCE/DOCKET NUMBER: P07 37217
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 213-622-7700
 - (B) TELEFAX: 213-489-4210

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGTAGCAA CGGAAACGGC GCGGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTG	60
TCGGCGGGCC TCCCCGCCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC	120
CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TCGTCCCCG CCGCGTTCCG	180
GCGTCTCCTT GCGCGGCCCC GCTCCCGGCT GTCCCCGCCC GCGGTGCGAG CCGGTGTATG	240
GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC	300
AGCAGCAACA GCAGCAGCAG CAGCAGCAG AGCCGCGGCC CGCGGCTGCC AATGTCGCA	360

CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys 150 155 160	654
CCC CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln 165 170 175 180	702
CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg 185 190 195	750
AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Pro Ser 200 205 210	798
CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro Ser Ser 215 220 225	846
GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly 230 235 240	894
CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly 245 250 255 260	942
ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly 265 270 275	990
TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val 280 285 290	1038
TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His 295 300 305	1086
GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu Ile Met 310 315 320	1134
GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys 325 330 335 340	1182
GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala 345 350 355	1230
ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro 360 365 370	1278
TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu 375 380 385	1326
AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn 390 395 400	1374
GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser 405 410 415 420	1422

TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg 425 430 435	1470
GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln 440 445 450	1518
TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu 455 460 465	1566
AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser 470 475 480	1614
ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg 485 490 495 500	1662
GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly 505 510 515	1710
CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser 520 525 530	1758
GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly 535 540 545	1806
GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro Pro Ser 550 555 560	1854
CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro 565 570 575 580	1902
ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser 585 590 595	1950
CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys 600 605 610	1998
CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg 615 620 625	2046
CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser 630 635 640	2094
GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT ACT CCT Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala Thr Pro 645 650 655 660	2142
CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA GTG GTC Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser Val Val 665 670 675	2190
AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro 680 685 690	2238

AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT GCT TCT Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu Ala Ser 695 700 705	2286
CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT ATT CCA Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro Ile Pro 710 715 720	2334
GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT GTT ACC Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Val Thr 725 730 735 740	2382
CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn 745 750 755	2430
TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA TCA CCT Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr Ser Pro 760 765 770	2478
AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT TCT GAA Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val Ser Glu 775 780 785	2526
CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT TTT AGG His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg 790 795 800	2574
TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA AAC AAA Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Asn Lys 805 810 815 820	2622
AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA ATT GAA Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Ile Glu 825 830 835	2670
CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC TGT ACC Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Ser Asn Cys Thr 840 845 850	2718
AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA ATA CTT Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser Ile Leu 855 860 865	2766
AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA GGG GTT Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val 870 875 880	2814
CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG GAA GAG Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys Glu Glu 885 890 895 900	2862
AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn 905 910 915	2910
GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr 920 925 930	2958
ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT ATG GTG Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser Met Val 935 940 945	3006
GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT TTT GCA Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys Phe Ala 950 955 960	3054

CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA CCT TTA Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln Pro Leu 965 970 975 980	3102
TAC CCA ATA CCT ATG ACG CCC ATG CCA GTG AAT CAA GCC AAG ACA TAT Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys Thr Tyr 985 990 995	3150
AGA GCA GTA CCA AAT ATG CCC CAA CAG CGG CAA GAC CAG CAT CAT CAG Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His His Gln 1000 1005 1010	3198
AGT GCC ATG ATG CAC CCA GCG TCA GCA GCG GGC CCA CCG ATT GCA GCC Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile Ala Ala 1015 1020 1025	3246
ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT CAG CAG Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro Gln Gln 1030 1035 1040	3294
TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG TCT CAG Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln Ser Gln 1045 1050 1055 1060	3342
CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA ATG ATG His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg Met Met 1065 1070 1075	3390
GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA GCA ACT Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ser Ala Thr 1080 1085 1090	3438
CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT CCC AAA Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys Pro Lys 1095 1100 1105	3486
TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC ATT TCC Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser 1110 1115 1120	3534
ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC CTG CAC Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His 1125 1130 1135 1140	3582
CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA CAG CAG Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln 1145 1150 1155	3630
CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT CAG CAC Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His 1160 1165 1170	3678
CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA CAG CAG His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln 1175 1180 1185	3726
CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC TCC ATG Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser Met 1190 1195 1200	3774
ACA CCT GCC TCC AAC ACG CAG TCG CCA CAG AAT AGT TTC CCA GCA GCA Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro Ala Ala 1205 1210 1215 1220	3822
CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG GCG TAT Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro Ala Tyr 1225 1230 1235	3870

ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA CAG TCA Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val Gln Ser 1240 1245 1250	3918
GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG CTA ATG Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met Leu Met 1255 1260 1265	3966
ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA AGT GCA Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln Ser Ala 1270 1275 1280	4014
CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT ATG ACG Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr Met Thr 1285 1290 1295 1300	4062
CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG TAAGGCTGCC His Pro Ser Val Gln Ala His His Gln Gln Gln Leu 1305 1310	4108
CTGGAGGAAC CGAAAGGCCA AATTCCTCC TCCCTTCTAC TGCTTCTACC AACTGGAAGC	4168
ACAGAAAAC AGAATTTTCAT TTATTTTGTT TTTAAAATAT ATATGTTGAT TTCTTGTAAC	4228
ATCCAATAGG AATGCTAACA GTTCACTTGC AGTGAAGAT ACTTGGACCG AGTAGAGGCA	4288
TTTAGGAACT TGGGGGCTAT TCCATAATTC CATATGCTGT TTCAGAGTCC CGCAGGTACC	4348
CCAGCTCTGC TTGCCGAAAC TGGAAGTTAT TTATTTTTTA ATAACCCTTG AAAGTCATGA	4408
ACACATCAGC TAGCAAAGA AGTAACAAGA GTGATTCTTG CTGCTATTAC TGCTAAAAAA	4468
AAAAAAAAAA AAA	4481

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu 1 5 10 15
Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln 20 25 30
Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly 35 40 45
Pro Tyr Pro Ser Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro 50 55 60
Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn 65 70 75 80
Gly Asn Gly Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly 85 90 95
Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala 100 105 110

Ser Pro Gly Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly
 115 120 125
 Ala Arg Ala Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala
 130 135 140
 Pro Gly Cys Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr
 145 150 155 160
 Met Ser Leu Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 165 170 175
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala
 180 185 190
 Ala Asn Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala
 195 200 205
 Ala Ala Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr
 210 215 220
 Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly
 225 230 235 240
 Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile
 245 250 255
 Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr
 260 265 270
 Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile
 275 280 285
 Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu
 290 295 300
 Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg
 305 310 315 320
 Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val
 325 330 335
 Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe
 340 345 350
 Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys
 355 360 365
 Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu
 370 375 380
 Glu Ala Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met
 385 390 395 400
 Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser
 405 410 415
 Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu
 420 425 430
 Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu
 435 440 445
 Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg
 450 455 460

Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg
 465 470 475 480
 Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly
 485 490 495
 Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser
 500 505 510
 Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr
 515 520 525
 Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val
 530 535 540
 Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser
 545 550 555 560
 Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg
 565 570 575
 Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser
 580 585 590
 Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser
 595 600 605
 Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro
 610 615 620
 Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly
 625 630 635 640
 Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu
 645 650 655
 Ala Ala Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp
 660 665 670
 Ser Ser Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg
 675 680 685
 Pro Arg Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro
 690 695 700
 Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala
 705 710 715 720
 Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn
 725 730 735
 Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp
 740 745 750
 Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn
 755 760 765
 Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro
 770 775 780
 Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys
 785 790 795 800
 Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln
 805 810 815

Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys
 820 825 830
 Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser
 835 840 845
 Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser
 850 855 860
 Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr
 865 870 875 880
 Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp
 885 890 895
 Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr
 900 905 910
 Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro
 915 920 925
 Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser
 930 935 940
 Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro
 945 950 955 960
 Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly
 965 970 975
 Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln
 980 985 990
 Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp
 995 1000 1005
 Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro
 1010 1015 1020
 Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr
 1025 1030 1035 1040
 Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His
 1045 1050 1055
 Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn
 1060 1065 1070
 Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser
 1075 1080 1085
 Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr
 1090 1095 1100
 Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr
 1105 1110 1115 1120
 Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn
 1125 1130 1135
 Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro
 1140 1145 1150
 Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser
 1155 1160 1165

Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala
 1170 1175 1180

Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr
 1185 1190 1195 1200

Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser
 1205 1210 1215

Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val
 1220 1225 1230

Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala
 1235 1240 1245

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro
 1250 1255 1260

Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu
 1265 1270 1275 1280

Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe
 1285 1290 1295

Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu
 1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

G CAC GAG GGG CCG CTC ACC ATG TCG CTG AAG CCG CAG CCG CAG CCG	46
His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro	
1 5 10 15	
CCC GCG CCC GCC ACT GGC CGC AAG CCC GGC GGC GGC CTG CTC TCG TCG	94
Pro Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser	
20 25 30	
CCC GGC GCC GCG CCG GCC TCG GCC GCG GTG ACC TCG GCT TCC GTG GTG	142
Pro Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val	
35 40 45	
CCG GCC CCG GCC GCG CCG GTG GCG TCT TCC TCG GCG GCC GCG GGC GGC	190
Pro Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly	
50 55 60	
GGG CGT CCC GGC CTG GGC AGA GGT CCG AAC AGT AGC AAA GGA CTG CCT	238

Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	Arg	Asn	Ser	Ser	Lys	Gly	Leu	Pro	
65						70					75					
CAG	CCT	ACG	ATT	TCT	TTT	GAT	GGA	ATC	TAT	GCA	AAC	GTG	AGG	ATG	GTT	286
Gln	Pro	Thr	Ile	Ser	Phe	Asp	Gly	Ile	Tyr	Ala	Asn	Val	Arg	Met	Val	
80					85					90					95	
CAT	ATA	CTT	ACG	TCA	GTT	GTT	GGA	TCG	AAA	TGT	GAA	GTA	CAA	GTG	AAA	334
His	Ile	Leu	Thr	Ser	Val	Val	Gly	Ser	Lys	Cys	Glu	Val	Gln	Val	Lys	
				100					105					110		
AAC	GGA	GGC	ATA	TAT	GAA	GGA	GTT	TTT	AAA	ACA	TAC	AGT	CCT	AAG	TGT	382
Asn	Gly	Gly	Ile	Tyr	Glu	Gly	Val	Phe	Lys	Thr	Tyr	Ser	Pro	Lys	Cys	
			115					120					125			
GAC	TTG	GTA	CTT	GAT	GCT	GCA	CAT	GAG	AAA	AGT	ACA	GAA	TCC	AGT	TCG	430
Asp	Leu	Val	Leu	Asp	Ala	Ala	His	Glu	Lys	Ser	Thr	Glu	Ser	Ser	Ser	
			130				135					140				
GGG	CCA	AAA	CGT	GAA	GAA	ATA	ATG	GAG	AGT	GTT	TTG	TTC	AAA	TGC	TCA	478
Gly	Pro	Lys	Arg	Glu	Glu	Ile	Met	Glu	Ser	Val	Leu	Phe	Lys	Cys	Ser	
	145					150					155					
GAC	TTC	GTT	GTG	GTA	CAG	TTT	AAA	GAT	ACA	GAC	TCC	AGT	TAT	GCA	CGG	526
Asp	Phe	Val	Val	Val	Gln	Phe	Lys	Asp	Thr	Asp	Ser	Ser	Tyr	Ala	Arg	
160					165					170					175	
AGA	GAT	GCT	TTT	ACT	GAC	TCT	GCT	CTC	AGC	GCA	AAG	GTG	AAT	GGT	GAG	574
Arg	Asp	Ala	Phe	Thr	Asp	Ser	Ala	Leu	Ser	Ala	Lys	Val	Asn	Gly	Glu	
				180					185					190		
CAC	AAG	GAG	AAG	GAC	CTG	GAG	CCC	TGG	GAT	GCA	GGG	GAG	CTC	ACG	GCC	622
His	Lys	Glu	Lys	Asp	Leu	Glu	Pro	Trp	Asp	Ala	Gly	Glu	Leu	Thr	Ala	
			195					200					205			
AGC	GAG	GAG	CTG	GAG	CTG	GAG	AAT	GAT	GTG	TCT	AAT	GGA	TGG	GAC	CCC	670
Ser	Glu	Glu	Leu	Glu	Leu	Glu	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	
			210				215					220				
AAT	GAC	ATG	TTT	CGA	TAT	AAT	GAA	GAG	AAT	TAT	GGT	GTG	GTG	TCC	ACA	718
Asn	Asp	Met	Phe	Arg	Tyr	Asn	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	
	225					230					235					
TAT	GAT	AGC	AGT	TTA	TCT	TCA	TAT	ACG	GTT	CCT	TTA	GAA	AGG	GAC	AAC	766
Tyr	Asp	Ser	Ser	Leu	Ser	Ser	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	
240					245					250					255	
TCA	GAA	GAA	TTT	CTT	AAA	CGG	GAG	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	814
Ser	Glu	Glu	Phe	Leu	Lys	Arg	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	
				260					265					270		
GAA	ATT	GAA	TCC	AGT	GCT	CAG	TAC	AAA	GCT	CGT	GTC	GCC	CTT	GAG	AAT	862
Glu	Ile	Glu	Ser	Ser	Ala	Gln	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	
			275					280					285			
GAT	GAC	CGG	AGT	GAG	GAA	GAA	AAA	TAC	ACA	GCA	GTC	CAG	AGA	AAC	TGC	910
Asp	Asp	Arg	Ser	Glu	Glu	Glu	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Cys	
		290					295					300				
AGT	GAC	CGG	GAG	GGG	CAT	GGC	CCC	AAC	ACT	AGG	GAC	AAT	AAA	TAT	ATT	958
Ser	Asp	Arg	Glu	Gly	His	Gly	Pro	Asn	Thr	Arg	Asp	Asn	Lys	Tyr	Ile	
	305					310					315					
CCT	CCT	GGA	CAA	AGA	AAC	AGA	GAA	GTC	CTA	TCC	TGG	GGA	AGT	GGG	AGA	1006
Pro	Pro	Gly	Gln	Arg	Asn	Arg	Glu	Val	Leu	Ser	Trp	Gly	Ser	Gly	Arg	
320					325					330					335	

CAG AGC TCA CCA CGG ATG GGC CAG CCT GGG CCA GGC TCC ATG CCG TCA Gln Ser Ser Pro Arg Met Gly Gln Pro Gly Pro Gly Ser Met Pro Ser 340 345 350	1054
AGA GCT GCT TCT CAC ACT TCA GAT TTC AAC CCG AAC GCT GGC TCA GAC Arg Ala Ala Ser His Thr Ser Asp Phe Asn Pro Asn Ala Gly Ser Asp 355 360 365	1102
CAA AGA GTA GTT AAT GGA GGT GTT CCC TGG CCA TCG CCT TGC CCA TCT Gln Arg Val Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser 370 375 380	1150
CCT TCC TCT CGC CCA CCT TCT CGC TAC CAG TCA GGT CCC AAC TCT CTT Pro Ser Ser Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu 385 390 395	1198
CCA CCT CGG GCA GCC ACC CCT ACA CGG CCT CGT GCC GAA TTC CTG CAG Pro Pro Arg Ala Ala Thr Pro Thr Arg Pro Arg Ala Glu Phe Leu Gln 400 405 410 415	1246
CCC GGG GAT CC Pro Gly Asp	1257

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Glu Gly Pro Leu Thr Met Ser Leu Lys Pro Gln Pro Gln Pro Pro 1 5 10 15
Ala Pro Ala Thr Gly Arg Lys Pro Gly Gly Gly Leu Leu Ser Ser Pro 20 25 30
Gly Ala Ala Pro Ala Ser Ala Ala Val Thr Ser Ala Ser Val Val Pro 35 40 45
Ala Pro Ala Ala Pro Val Ala Ser Ser Ser Ala Ala Ala Gly Gly Gly 50 55 60
Arg Pro Gly Leu Gly Arg Gly Arg Asn Ser Ser Lys Gly Leu Pro Gln 65 70 75 80
Pro Thr Ile Ser Phe Asp Gly Ile Tyr Ala Asn Val Arg Met Val His 85 90 95
Ile Leu Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn 100 105 110
Gly Gly Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp 115 120 125
Leu Val Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly 130 135 140
Pro Lys Arg Glu Glu Ile Met Glu Ser Val Leu Phe Lys Cys Ser Asp 145 150 155 160

Phe Val Val Val Gln Phe Lys Asp Thr Asp Ser Ser Tyr Ala Arg Arg
 165 170 175
 Asp Ala Phe Thr Asp Ser Ala Leu Ser Ala Lys Val Asn Gly Glu His
 180 185 190
 Lys Glu Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Ser
 195 200 205
 Glu Glu Leu Glu Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn
 210 215 220
 Asp Met Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr
 225 230 235 240
 Asp Ser Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser
 245 250 255
 Glu Glu Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu
 260 265 270
 Ile Glu Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp
 275 280 285
 Asp Arg Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Cys Ser
 290 295 300
 Asp Arg Glu Gly His Gly Pro Asn Thr Arg Asp Asn Lys Tyr Ile Pro
 305 310 315 320
 Pro Gly Gln Arg Asn Arg Glu Val Leu Ser Trp Gly Ser Gly Arg Gln
 325 330 335
 Ser Ser Pro Arg Met Gly Gln Pro Gly Pro Gly Ser Met Pro Ser Arg
 340 345 350
 Ala Ala Ser His Thr Ser Asp Phe Asn Pro Asn Ala Gly Ser Asp Gln
 355 360 365
 Arg Val Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro
 370 375 380
 Ser Ser Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro
 385 390 395 400
 Pro Arg Ala Ala Thr Pro Thr Arg Pro Arg Ala Glu Phe Leu Gln Pro
 405 410 415
 Gly Asp